2877

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re application of: Gibson et al.

Application No.: 09/580,380

Filed: May 26, 2000

Title: METHOD OF DETERMINING THE THREE-DIMENSIONAL SHAPE OF A MACROMOLECULE

Attorney Docket No.: UCSFP001/1584.002

Examiner: Unknown

Group: 2877

CERTIFICATE OF MAILING

I hereby certify that this correspondence is being deposited with the United States Postal Service as First Class Mail to: Commissioner for Patents, Washington, DC 20231 on August 7, 2001.

Signed: Leslie Russell

Leslie Russell

INFORMATION DISCLOSURE STATEMENT
37 CFR §§1.56 AND 1.97(b)

Commissioner for Patents
Washington, DC 20231

Dear Sir:

The references listed in the attached PTO Form 1449, copies of which are attached, may be material to examination of the above-identified patent application. Applicants submit these references in compliance with their duty of disclosure pursuant to 37 CFR §§1.56 and 1.97. The Examiner is requested to make these references of official record in this application.

The Applicants have only submitted the title of document 4B and some correspondence with the author and have no further material available. This Information Disclosure Statement is not to be construed as a representation that a search has been made, that additional information material to the examination of this application does not exist, or that these references indeed constitute prior art.

This Information Disclosure Statement is: (i) filed within three (3) months of the filing date of the above-referenced application, (ii) believed to be filed before the mailing date of a first Office Action on the merits, or (iii) believed to be filed before the mailing of a first Office Action after the filing of a Request for Continued Examination under §1.114. Accordingly, it is believed that no fees are due in connection with the filing of this Information Disclosure Statement. However, if it is determined that any fees are due, the Commissioner is hereby

authorized to charge such fees to Deposit Account 500388 (Order No. UCSFP001).

Respectfully submitted,
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U.S. Patent Documents

Examiner Initial	No.	Patent No.	Date	Patentee	Class	Sub-class	Filing Date
CR	1A	5,045,694	09/03/91	Beavis *et al.*			09/27/89
CR	1B	5,160,840	11/03/92	Vestal			10/25/91
CR	1C	5,627,369	05/06/97	Vestal *et al.*			06/07/95
	1D						
	1E						
	1F						

Foreign Patent or Published Foreign Patent Application

Examiner Initial	No.	Document No.	Publication Date	Country or Patent Office	Class	Sub-class	Translation Yes	Translation No
	1J							
	1K							
	1L							

Other Documents

Examiner Initial	No.	Author, Title, Date, Place (e.g. Journal) of Publication
CR	1O	Cohen et al. "On the Use of Chemically Derived Distance Constraints in the Prediction of Protein Structure with Myoglobin as an Example." J Mol. Biol. 1980 137:9-22
	1P	Mitra et al. "Reagents for the cross-linking of proteins by equilibrium transfer alkylation." J Am. Chem. Soc. 1979 101, 3097. For example, amino acid surface accessibility in proteins has been probed using selective chemical modifications followed by proteolytic digestion and mass spectrometry profiling, of the resulting modified (and unmodified) peptides
	1Q	Suckau et al. "Protein surface topology-probing by selective chemical modification and mass spectrometric peptide mapping." Proc Natl Acad Sci USA. 1992 Jun 15;89(12):5630-4
Examiner		Date Considered 8/11/03

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Other Documents

Examiner Initial	No.	Author, Title, Date, Place (e.g. Journal) of Publication
CM	2A	Glocker et al. "Molecular characterization of surface topology in protein tertiary structures by amino-acylation and mass spectrometric peptide mapping." Bioconjug. Chem. 1994 Nov-Dec;5(6):583-90
	2B	Seielstad et al. "Analysis of the structural core of the human estrogen receptor ligand binding domain by selective proteolysis/mass spectrometric analysis." Biochemistry. 1995 Oct 3;34(39):12605-15
	2C	Seielstad et al. "Molecular characterization by mass spectrometry of the human estrogen receptor ligand-binding domain expressed in Escherichia Coli." Mol. Endocrinol. 1995 Jun;9(6):647-58
	2D	Zappacosta et al. "Surface Topology of Minibody by Selective Chemical Modifications and Mass Spectrometry." Protein Sci. 1997 Sep;6(9):1901-9
	2E	Scaloni, et al. "Structural investigations on human erythrocyte acylpeptide hydrolase by mass spectrometric procedures." J Protein Chem. 1999 Apr;18(3):349-60
	2F	Smith et al. "Probing the non-covalent structure of proteins by amide hydrogen exchange and mass spectrometry." J Mass. Spectrom. 1979 32(2): 135-146. 1997
	2G	Papac et al. "Epitope mapping of the gastrin-releasing peptide/anti-bombesin monoclonal antibody complex by proteolysis followed by matrix-assisted laser desorption ionization mass spectrometry." Protein Sci. 1994 Sep;3(9):1485-92
	2H	Cohen et. al. "Probing the solution structure of the DNA-binding protein Max by a combination of proteolysis mass spectrometry." Protein Sci. 1995 Jun;4(6):1088-99
	2I	Gomes et al. "Proteolytic mapping of human replication protein A: evidence for multiple structural domains and a conformational change upon interaction with single-stranded DNA. Biochemistry. 1996 Apr 30;35(17):5586-95
	2J	Zappacosta et al. "Probing the tertiary structure of proteins by limited proteolysis and mass spectrometry: the case of Minibody." Protein Sci. 1996 May;5(5):802-13

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Other Documents

Examiner Initial	No.	Author, Title, Date, Place (e.g. Journal) of Publication
opc	3A	Gervasoni et al. "Identification of the binding surface on beta-lactamase for GroEL by limited proteolysis and MALDI-mass spectrometry." Biochemistry. 1998 Aug 18;37(33):11660-9
	3B	Moore et al. "Proteolytic fragments of the nicotinic acetylcholine receptor identified by mass spectrometry: implications for receptor topography." Biochemistry. 1989 Nov 14;28(23):9184-91
	3C	Massotte D, et al. "Structure of the membrane-bound form of the pore-forming domain of colicin A: a partial proteolysis and mass spectrometry study." Biochemistry. 1993 Dec 21;32(50):13787-94
	3D	Havel et al. "Effects of Distance Constraints on Macromolecular Conformation. II. Simulation of Experimental Results and Theoretical Predictions." Biopolymers. 1979 18:73-81
	3E	Lacroix et al. "Structure and assembly of the catalytic region of human complement protease C1r: a three-dimensional model based on chemical cross-linking and homology modeling." Biochemistry. 1997 May 27;36(21):6270-82
	3F	Dyda et al. "Crystal structure of the catalytic domain of HIV-1 integrase: similarity to other polynucleotidyl transferases." Science. 1994 Dec 23;266(5193):1981-6;
	3G	Lodi et. al. "Solution structure of the DNA binding domain of HIV-1 integrase." Biochemistry. 1995 Aug 8;34(31):9826-33
	3H	Goldgur et. al. "Three new structures of the core domain of HIV-1 integrase: an active site that binds magnesium." Proc Natl Acad Sci USA. 1998 Aug 4;95(16):9150-4
	3I	Havel et al. "An evaluation of the combined use of nuclear magnetic resonance and distance geometry for the determination of protein conformations in solution." J Mol Biol. 1985 Mar 20;182(2):281-94
	3J	Guntert et al. "Improved efficiency of protein structure calculations from NMR data using the program DIANA with redundant dihedral angle constraints." J Biomol NMR. 1991 Nov;1(4):447-56
	3K	Grant et al., "Edman Sequencing as Tool for Characterization of Synthetic Peptides." Methods Enzymol. 1997 289:395-419

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CR	4A	Lennon et. al., Proceedings of the 42nd ASMS Conference on Mass Spectrometry and Allied Topics, May 29-Jun. 3, 1994, Chicago, Illinois, p. 501
	4B	Breuker et al., 13th International Mass Spectrometry Conference, Aug. 29-Sep. 3, 1994, Budapest, Hungary
	4C	Reilly et al., "Improving the Resolution of Matrix-assisted Laser Desorption/Ionization Time-of-flight Mass Spectrometry by Exploiting the Correlation between Ion Position and Velocity," Rapid Commun., Mass Spectrometry, 8, 1994, 865-868
	4D	Fenn et al., "Electrospray Ionization-Principle and Practice," Mass Spectrom. Rev., vol. 9, pp. 37-70 (1990)
	4E	P. Kebarle et al., "From Ions in Solution to Ions in the Gas Phase," Anal. Chem.65: 972A-986A (1993)
	4F	Havel, et al. "The Combinatorial Distance Geometry Method for the Calculation of Molecular Conformation. I. A New Approach to an Old Problem", J Theor Biol. 104:359-81 (1983)
	4G	Alexandrov et al. "Fast Protein Fold Recognition via Sequence to Structure Alignment and Contact Capacity Potentials." Protein Science Bulletin. (1996)
	4H	Bryant et al. "An Empirical Energy Function for Threading Protein Sequence Through the Folding Motif," Proteins. 1993 16 92-112
	4I	Murzin et al. "SCOP: a Structural Classification of Proteins Database for the Investigation of Sequences and Structures." J Mol Biol. 1995 Apr 7;247(4):536-40
	4J	Venkataraman et al. "Preferential self-association of basic fibroblast growth factor is stabilized by heparin during receptor dimerization and activation." Proc Natl Acad Sci USA. 1996 Jan 23;93(2):845-50
	4K	Haniu et al. "Recombinant human erythropoietin (rHuEPO): cross-linking with disuccinimidyl esters and identification of the interfacing domains in EPO." Protein Sci. 1993 Sep;2(9):1441-51
	4L	Laemmli. "Cleavage of structural proteins during the assembly of the head of bacteriophage T4." Nature. 1970 Aug 15;227(259):680-5
	4M	Kaufmann et al. "Mass spectrometric sequencing of linear peptides by product-ion analysis in a reflectron time-of-flight mass spectrometer using matrix-assisted laser desorption ionization." Rapid Commun Mass Spectrom. 1993 Oct;7(10):902-10

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Examiner Initial	No.	Author, Title, Date, Place (e.g. Journal) of Publication
CDL	5A	Holm et al. "Protein Structure Comparison by Alignment of Distance Matrices." J Mol Bio. 1993 233:123-38
	5B	Hilbert et al. "Structural relationships of homologous proteins as a fundamental principle in homology modeling." Proteins. 1993 17(2):138-51
	5C	Tullius et. al. "Covalent modification of Lys19 in the CTP binding site of cytidine 5'-monophosphate N-acetylneuraminic acid synthetase." Protein Sci. 1999 Mar;8(3):666-75
	5D	Samules, et al. "Investigation of the Kinetic Mechanism of Cytidine 5'-Monophosphate N-Acetylneuraminic Acid Synthetase from Haemophilus ducreyi With New Insights On Rate-limiting Steps from Product Inhibition Analysis." Biochemistry. 1999 38(19) 6195-203
	5E	Rossi et al. "Structure of the catalytic region of human complement protease C1s: study by chemical cross-linking and three-dimensional homology modeling." Biochemistry. 1995 Jun 6;34(22):7311-21

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